

Sequence length 2175

CACCGCGTCEGCAAATTCTGATTCTTGAATTAGGATTCAGATGGGGCCTCATTTCTACAGCCCCAACATTCT
ATAGCCGTTATCACTGCCATCACCACTGCCACCAACATCTCTGAGATTCACCCCCCTGCTCCCCAGAGACTTCCTGC
TTTGAAGTGGCAGAAAGGAAGCTCTAGTGGTGGCTGCGCTCCAGACAATCGGAATCCCTGC

M G W L F L K V L L A G V S F S G	17
CTTCACCACC ATG GGC TGG CTT TTT CTA AAG GTT TTG GCG GGA GTG AGT TTC TCA GGA	51
F L Y P L V D F C I S G K T R G Q K P N	37
TTT CTT TAT CCT CTT GTG GAT TTT TGC ATC AGT GGG AAA ACA AGA GGA CAG AAG CCA AAC	111
F V I I L A D D M G W G D L G A N W A E	57
TTT GTG ATT ATT TTG GCC GAT GAC ATG GGG TGG GGT GAC CTG GGA GCA AAC TGG GCA GAA	171
T K D T A N L D K M A S E G M R F V D F	77
ACA AAG GAC ACT GCC AAC CTT GAT AAG ATG GCT TCG GAG GGA ATG AGG TTT GTG GAT TTC	231
H A A A S T C S P S R A S L L T G R L G	97
CAT GCA GCT GCC TCC ACC TGC TCA CCC TCC CGG GCT TCC TTG CTC ACC GGC CGG CTT GGC	291
L R N G V T R N F A V T S V G G L P L N	117
CTT CGC AAT GGA GTC ACA CGC AAC TTT GCA GTC ACT TCT GTG GGA GGC CTT CCG CTC AAC	351
E T T L A E V L Q Q A G Y V T G I I G K	137
GAG ACC ACC TTG GCA GAG GTG CTG CAG GCG GGT TAC GTC ACT GGG ATA ATA GGC AAA	411
W H L G H H G S Y H P N F R G F D Y Y F	157
TGG CAT CTT GGA CAC CAC GGC TCT TAT CAC CCC AAC TTC CGT GGT TTT GAT TAC TAC TTT	471
G I P Y S H D M G C T D T P G Y N H P P	177
GGA ATC CCA TAT AGC CAT GAT ATG GGC TGT ACT GAT ACT CCA GGC TAC AAC CAC CCT CCT	531
C P A C P Q G D G P S R N L Q R D C Y T	197
TGT CCA GCG TGT CCA CAG GGT GAT GGA CCA TCA AGG AAC CTT CAA AGA GAC TGT TAC ACT	591
D V A L P L Y E N L N I V E Q P V N L S	217
GAC GTG GCC CTC CCT CTT TAT GAA AAC CTC AAC ATT GTG GAG CAG CCG GTG AAC TTG AGC	651
S L A Q K Y A E K A T Q F I Q R A S T S	237
AGC CTT GCC CAG AAG TAT GCT GAG AAA GCA ACC CAG TTC ATC CAG CGT GCA AGC ACC AGC	711
G R P F L L Y V A L A H M H V P L P V T	257
GGG AGG CCC TTC CTG CTC TAT GTG GCT CTG GGC CAC ATG CAC GTG CCC TTA CCC GTG ACT	771
Q L P A A P R G R S L Y G A G L W E M D	277
CAG CTA CCA GCA GCG CCA CGG GGC AGA AGC CTG TAT GGT GCA GGG CTC TGG GAG ATG GAC	831
S L V G Q I K D K V D H T V K E N T F L	297
AGT CTG GTG GGC CAG ATC AAG GAC AAA GTT GAC CAC ACA GTG AAG GAA AAC ACA TTC CTC	891
W F T G D N G P W A Q K C E L A G S V G	317
TGG TTT ACA GGA GAC AAT GGC CCG TGG GCT CAG AAG TGT GAG CTA GCG GGC AGT GTG GGT	951
P F T G F W Q T R Q G G S P A K Q T T W	337
CCC TTC ACT GGA TTT TGG CAA ACT CGT CAA GGG GGA AGT CCA GCC AAG CAG ACG ACC TGG	1011
E G G H R V P A L A Y W P G R V P V N V	357

GAA GGA GGG CAC CGG GTC CCA GCA CTG GCT TAC TGG CCT GGC AGA GTT CCA GTT AAT GTC 1071
 T S T A L L S V L D I F P T V V A L A Q 377
 ACC AGC ACT GCC TTG TTA AGC GTG CTG GAC ATT TTT CCA ACT GTG GTA GCC CTG GCC CAG 1131
 A S L P Q G R R F D G V D V S E V L F G 397
 GCC AGC TTA CCT CAA GGA CGG CGC TTT GAT GGT GTG GAC GTC TCC GAG GTG CTC TTT GGC 1191
 R S Q P G H R V L F H P N S G A A G E F 417
 CGG TCA CAG CCT GGG CAC AGG GTG CTG TTC CAC CCC AAC AGC GGG GCA GCT GGA GAG TTT 1251
 G A L Q T V R L E R Y K A F Y I T G G A 437
 GGA GCC CTG CAG ACT GTC CGC CTG GAG CGT TAC AAG GCC TTC TAC ATT ACC GGT GGA GCC 1311
 R A C D G S T G P E L Q H K F P L I F N 457
 AGG GCG TGT GAT GGG AGC ACG GGG CCT GAG CTG CAG CAT AAG TTT CCT CTG ATT TTC AAC 1371
 L E D D T A E A V P L E R G G A E Y Q A 477
 CTG GAA GAC GAT ACC GCA GAA GCT GTG CCC CTA GAA AGA GGT GGT GCG GAG TAC CAG GCT 1431
 V L P E V R K V L A D V L Q D I A N D N 497
 GTG CTG CCC GAG GTC AGA AAG GTT CTT GCA GAC GTC CTC CAA GAC ATT GCC AAC GAC AAC 1491
 I S S A D Y T Q D P S V T P C C N P Y Q 517
 ATC TCC AGC GCA GAT TAC ACT CAG GAC CCT TCA GTA ACT CCC TGC TGT AAT CCC TAC CAA 1551
 I A C R C Q A A * 526
 ATT GCC TGC CGC TGT CAA GCC GCA TAA 1578

CAGACCAATTTTATTCCACGAGGAGGAGTACCTGAAATTAGGAAGTTGCTTCAAATTTCATTTTACCCCTTT
 ACAAAACACACGCTTAGTTAGCTTGGAGTTAGTTTGGAGTTAGCCTGCAATATCCCTCTGTATCCTGTCCCTCC
 TCCACGCGACCCGAGAGCAGCTGAGCTGCGCTGGCTCTGGCAGGGAGTGTGCCTTAATGGGAAGCACACGGGCTTG
 GAGTCAGGCACAGGTGCCAGCTCCAGCTTGAACCTGGCAATTGTTAACCTAACCTGCAAGTTGATTTGAGGGTT
 AAATAAAGGCATACATGAAAAAAAAAAAAAAA

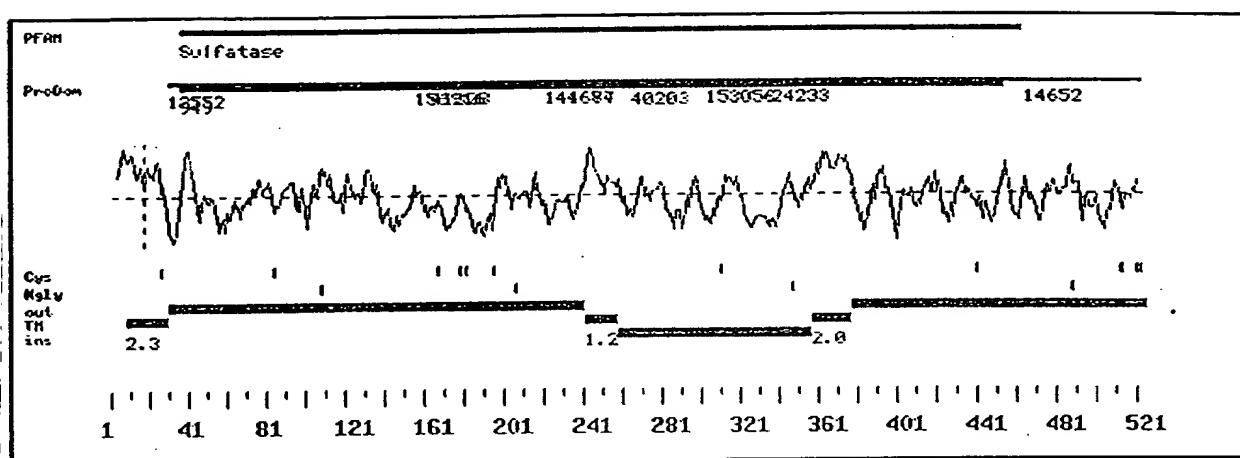


FIG 2

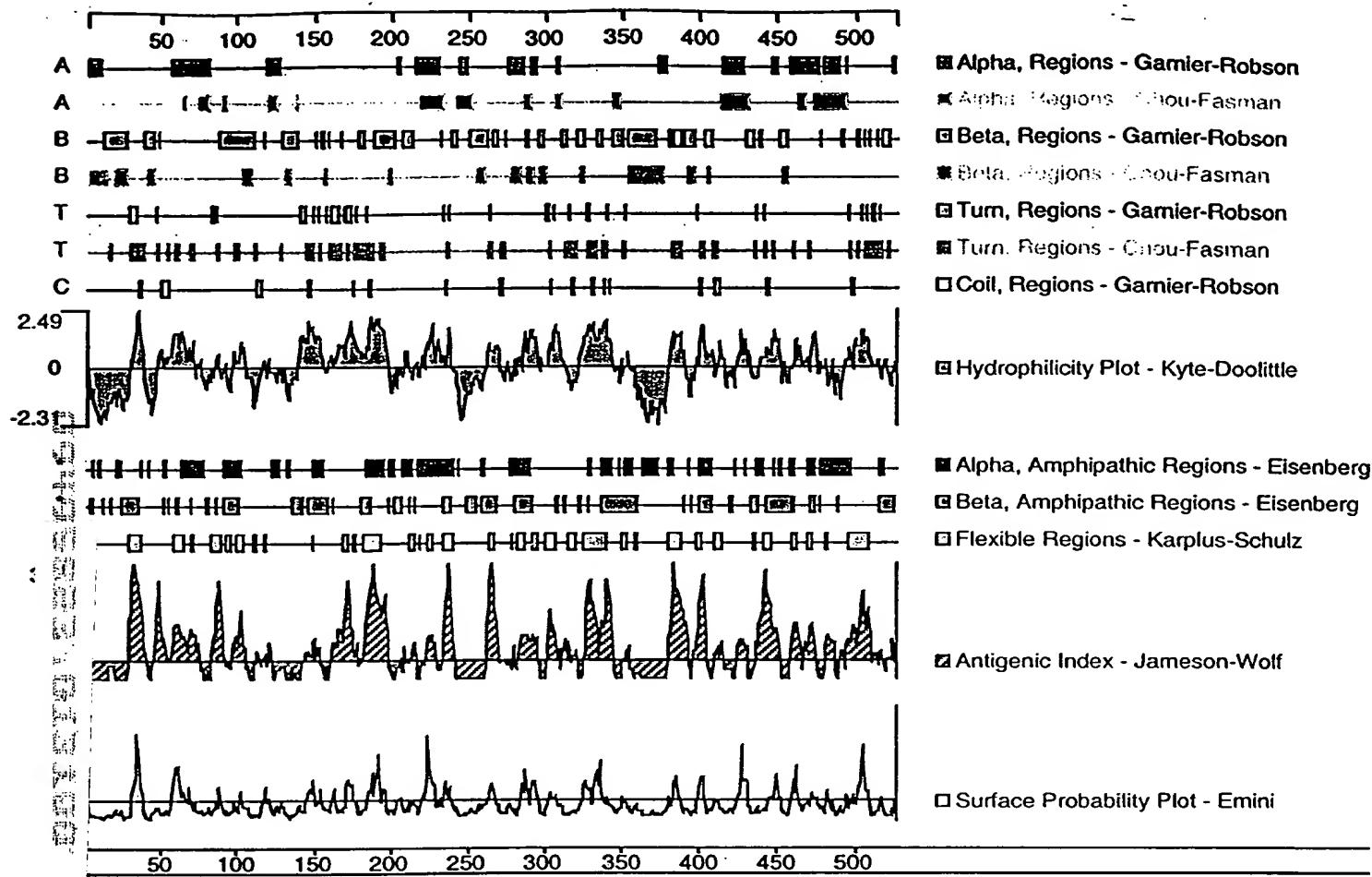


FIG 3

Prosite Pattern Matches :

Prosite version: Release 12.2 of February 1995

>PS00001|PDOC00001|ASN_GLYCOSYLATION N-glycosylation site.

Query: 117	NETT	120
Query: 215	NLSS	218
Query: 356	NVTS	359
Query: 497	NISS	500

>PS00005|PDOC00005|PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.

Query: 28	SGK	30
Query: 93	TGR	95
Query: 237	SGR	239
Query: 290	TVK	292
Query: 422	TVR	424

>PS00006|PDOC00006|CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

Query: 120	TLAE	123
Query: 290	TVKE	293
Query: 335	TTWE	338
Query: 364	SVLD	367
Query: 444	TGPE	447
Query: 499	SSAD	502

>PS00008|PDOC00008|MYRISTYL N-myristoylation site.

Query: 12	GVSFSG	17
Query: 33	GQKPNF	38
Query: 52	GANWAE	57
Query: 97	GLRNGV	102
Query: 113	GLPLNE	118
Query: 158	GIPYSH	163
Query: 328	GGSPAK	333
Query: 388	GVDVSE	393
Query: 418	GALQTV	423
Query: 435	GGARAC	440

>PS00009|PDOC00009|AMIDATION Amidation site.

Query: 382 QGRR 385

>PS00142|PDOC00117|SULFATASE_2 Sulfatases signature 2.

Query: 129 GYVTGIIIGKW 138

FIG 4

Input file Fbh23553f1.seq; Output File 23553.trans
Sequence length 4321

CCOAOGOGTCGGCTAATGAATCTGGGGCOGGTGTGGGCGGGGGCGCTTGATCGGCAACTAGGAAACCCAGGCG
AGAGGCCAGGAGCGAGGCAGCGAGGATCAGAGGCCAGGCCTCCCGGCTGCGGGCGCTCCCTGGAGGTCAAGGGCAGAT
GAGGAACATGACTCTCCCCCTTCGGAGGAGGAAGGAAGTCCCGCTGCCACCTTATCTCTGCTOCTCTGCTCCCTCCCTG
TTCAGAGCTTTCTAGAGAAGATTTGAAGGCGCTTTTGCTGACGGCCACCCACCATCATCTAAAGAAGAT
AAACTGGCAAATGACATGCAGGTTCTCAAGGAGAATAATTGAGAAAATCTCAAAAGGACCTATCTGCAGATGTT
CTGAATACCTCTGAGAATAGAGATTGATTATTCAACCAGGATACTTAAGAACCTCAGAAAATCAGGAGACGGAGA

M	K	Y	S	C	C	A	L	V	L	A	11									
CATTTTGTCAGTTTGCAACATGGACCAAATACA											ATG AAG TAT TCT TGC TGT GCT CTG GTT TTG GCT	33								
V	L	G	T	E	L	L	G	S	L	C	S	T	V	R	S	P	R	F	R	31
GTC CTG GGC ACA GAA TTG CTG GGA AGC CTC TGT TCG ACT GTC AGA TCC CCG AGG TTC AGA											93									
G	R	I	Q	Q	E	R	K	N	I	R	P	N	I	I	L	V	L	T	D	51
GGA CGG ATA CAG CAG GAA CGA AAA AAC ATC CGA CCC AAC ATT ATT CTT GTG CTT ACC GAT											153									
<u>D</u>	<u>Q</u>	D	V	E	L	G	S	L	Q	V	M	N	K	T	R	K	I	M	E	71
GAT CAA GAT GTG GAG CTG GGG TCC CTG CAA GTC ATG AAC AAA ACG AGA AAG ATT ATG GAA											213									
H	G	G	A	T	F	I	N	A	F	V	T	T	P	M	<u>C</u>	<u>C</u>	P	S	R	91
CAT GGG GGG GCC ACC TTC ATC AAT GCC TTT GTG ACT ACA CCC ATG TGC TGC CCG TCA CGG											273									
S	S	M	L	T	G	K	<u>Y</u>	V	H	N	H	N	V	Y	T	N	N	E	N	111
TCC TCC ATG CTC ACC GGG AAG TAT GTG CAC AAT CAC AAT GTC TAC ACC AAC AAC GAG AAC											333									
C	S	S	P	S	W	Q	A	M	H	E	P	R	T	F	A	V	Y	L	N	131
TGC TCT TCC CCC TCG TGG CAG GCC ATG CAT GAG CCT CGG ACT TTT GCT GTA TAT CTT AAC											393									
N	T	<u>G</u>	<u>Y</u>	R	T	A	F	F	<u>G</u>	<u>K</u>	<u>Y</u>	L	N	E	<u>Y</u>	N	<u>G</u>	<u>S</u>	<u>Y</u>	151
AAC ACT GGC TAC AGA ACA GCC TTT TTT GGA AAA TAC CTC AAT GAA TAT AAT GGC AGC TAC											453									
<u>I</u>	<u>P</u>	<u>P</u>	<u>G</u>	<u>W</u>	R	E	W	L	G	L	I	K	N	S	R	<u>F</u>	<u>Y</u>	N	<u>Y</u>	171
ATC CCC CCT GGG TGG CGA GAA TGG CTT GGA TTA ATC AAG AAT TCT CGC TTC TAT AAT TAC											513									
T	V	C	R	N	G	I	K	E	K	H	G	F	D	Y	A	<u>K</u>	<u>D</u>	<u>Y</u>	F	191
ACT GTT TGT CGC AAT GGC ATC AAA GAA AAG CAT GGA TTT GAT TAT GCA AAG GAC TAC TTC											573									
T	<u>D</u>	L	I	T	N	E	S	I	N	Y	F	K	M	S	K	R	M	Y	P	211
ACA GAC TTA ATC ACT AAC GAG AGC ATT AAT TAC TTC AAA ATG TCT AAG AGA ATG TAT CCC											633									
H	R	P	V	M	M	V	I	S	H	A	<u>A</u>	<u>P</u>	H	G	<u>P</u>	<u>E</u>	D	S	A	231
CAT AGG CCC GTT ATG ATG GTG ATC AGC CAC GCT GCG CCC CAC GGC CCC GAG GAC TCA GCC											693									
P	Q	F	S	K	L	Y	P	N	A	S	Q	H	I	T	P	S	Y	N	Y	251
CCA CAG TTT TCT AAA CTG TAC CCC AAT GCT TCC CAA CAC ATA ACT CCT AGT TAT AAC TAT											753									
A	P	N	M	D	K	H	W	I	M	Q	Y	T	G	P	M	L	P	I	H	271
GCA CCA AAT ATG GAT AAA CAC TGG ATT ATG CAG TAC ACA GGA CCA ATG CTG CCC ATC CAC											813									
M	E	F	T	N	I	L	Q	R	<u>K</u>	<u>R</u>	<u>L</u>	<u>Q</u>	<u>T</u>	<u>L</u>	M	S	V	D	D	291
ATG GAA TTT ACA AAC ATT CTA CAG CGC AAA AGG CTC CAG ACT TTG ATG TCA GTG GAT GAT											873									
S	V	E	R	L	Y	N	M	L	V	E	T	G	E	L	E	N	T	Y	I	311

FIG 5 (-1-)

TCT GTG GAG AGG CTG TAT AAC ATG CTC GTG GAG ACG GGG GAG CTG GAG AAT ACT TAC ATC 933
 I Y T A D H G Y H I G Q F G L V K G K S 331
 ATT TAC ACC GCC GAC CAT GGT TAC CAT ATT GGG CAG TTT GGA CTG GTC AAG GGG AAA TCC 993
 M P Y D F D I R V P F F I R G P S V E P 351
 ATG CCA TAT GAC TTT GAT ATT CGT GTG CCT TTT ATT CGT GGT CCA AGT GTA GAA CCA 1053
 G S I V P Q I V L N I D L A P T I L D I 371
 GGA TCA ATA GTC CCA CAG ATC GTT CTC AAC ATT GAC TTG GCC CCC ACG ATC CTG GAT ATT 1113
 A G L D T P P D V D G K S V L K L L D P 391
 GCT GGG CTC GAC ACA CCT CCT GAT GTG GAC GGC AAG TCT GTC CTC AAA CTT CTG GAC CCA 1173
 E K P G N R F R T N K K A K I W R D T F 411
 GAA AAG CCA GGT AAC AGG TTT CGA ACA AAC AAG AAG GCC AAA ATT TGG CGT GAT ACA TTC 1233
 L V E R G K F L R K K E E S S K N I Q Q 431
 CTA GTG GAA AGA GGC AAA TTT CTA CGT AAG AAG GAA GAA TCC AGC AAG AAT ATC CAA CAG 1293
 S N H L P K Y E R V K E L C Q Q A R Y Q 451
 TCA AAT CAC TTG CCC AAA TAT GAA CGG GTC AAA GAA CTA TGC CAG CAG GCC AGG TAC CAG 1353
 T A C E Q P G Q K W Q C I E D T S G K L 471
 ACA GCC TGT GAA CAA CCG GGG CAG AAG TGG CAA TGC ATT GAG GAT ACA TCT GGC AAG CTT 1413
 R I H K C K G P S D L L T V R Q S T R N 491
 CGA ATT CAC AAG TGT AAA GGA CCC AGT GAC CTG CTC ACA GTC CGG CAG AGC ACG CGG AAC 1473
 L Y A R G F H D K D K E C S C R E S G Y 511
 CTC TAC GCT CGC GGC TTC CAT GAC AAA GAC AAA GAG TGC AGT TGT AGG GAG TCT GGT TAC 1533
 R A S R S Q R K S Q R Q F L R N Q G T P 531
 CGT GCC AGC AGA AGC CAA AGA AAG AGT CAA CGG CAA TTC TTG AGA AAC CAG GGG ACT CCA 1593
 K Y K P R F V H T R Q T R S L S V E F E 551
 AAG TAC AAG CCC AGA TTT GTC CAT ACT CGG CAG ACA CGT TCC TTG TCC GTC GAA TTT GAA 1653
 G E I Y D I N L E E E E L Q V L Q P R 571
 GGT GAA ATA TAT GAC ATA AAT CTG GAA GAA GAA TTG CAA GTG TTG CAA CCA AGA 1713
 N I A K R H D E G H K G P R D L Q A S S 591
 AAC ATT GCT AAG CGT CAT GAT GAA GGC CAC AAG GGG CCA AGA GAT CTC CAG GCT TCC AGT 1773
 G G N R G R M L A D S S N A V G P P T T 611
 GGT GGC AAC AGG GGC AGG ATG CTG GCA GAT AGC AAC GCC GTG GGC CCA CCT ACC ACT 1833
 V R V T H K C F I L P N D S I H C E R E 631
 GTC CGA GTG ACA CAC AAG TGT TTT ATT CTT CCC AAT GAC TCT ATC CAT TGT GAG AGA GAA 1893
 L Y Q S A R A W K D H K A Y I D K E I E 651
 CTG TAC CAA TCG GCC AGA GCG TGG AAG GAC CAT AAG GCA TAC ATT GAC AAA GAG ATT GAA 1953
 A L Q D K I K N L R E V R G H L K R R K 671
 GCT CTG CAA GAT AAA ATT AAG AAT TTA AGA GAA GTG AGA GGA CAT CTG AAG AGA AGG AAG 2013
 P E E C S C S K Q S Y Y N K E K G V K K 691
 CCT GAG GAA TGT AGC TGC AGT AAA CAA AGC TAT TAC ATT AAA GAG AAA GGT GTA AAA AAG 2073
 Q E K L K S H L H P F K E A A Q E V D S 711
 CAA GAG AAA TTA AAG AGC CAT CTT CAC CCA TTC AAG GAG GCT GCT CAG GAA GTA GAT AGC 2133

K L Q L F K E N N R R R K K K E R K E K R	731
AAA CTG CAA CTT TTC AAG GAG AAC AAC CGT AGG AGG AAG AAG GAG AGG AAG GAG AAG AGA	2193
R Q R K G E E C S L P G L T C F T H D N	751
CGG CAG AGG AAG GGG GAA GAG TGC AGC CTG CCT GGC CTC ACT TGC TTC AGC CAT GAC AAC	2253
N H W Q T A P F W N L G S F C A C T S S	771
AAC CAC TGG CAG ACA GCC CCG TTC TGG AAC CTG GGA TCT TTC TGT GCT TGC ACG AGT TCT	2313
N N N T Y W C L R T V N E T H N F L F C	791
AAC AAT AAC ACC TAC TGG TGT TTG CGT ACA GTT AAT GAG ACG CAT AAT TTT CTT TTC TGT	2373
E F A T G F L E Y F D M N T D P Y Q L T	811
GAG TTT GCT ACT GCC TTT TTG GAG TAT TTT GAT ATG AAT ACA GAT CCT TAT CAG CTC ACA	2433
N T V H T V E R G I L N Q L H V Q L M E	831
AAT ACA GTG CAC ACG GTA GAA CGA GGC ATT TTG AAT CAG CTA CAC GTA CAA CTA ATG GAG	2493
L R S C Q G Y K Q C N P R P K N L D V G	851
CTC AGA AGC TGT CAA GGA TAT AAG CAG TGC AAC CCA AGA CCT AAG AAT CTT GAT GTT GGA	2553
N K D G G S Y D L H R G Q L W D G W E G	871
AAT AAA GAT GGA GGA AGC TAT GAC CTA CAC AGA GGA CAG TTA TGG GAT GGA TGG GAA GGT	2613
*	872
TAA	2616
TCAGCCCCGTCTCACTGCAGACATCAACTGGCAAGGCCTAGAGGAGCTACACAGTGTGAATGAAAACATCTATGAGTAC AGACAAAAACTACAGACTTAGTCTGGTGGACTGGACTAATTACTTGAAGGATTAGATAGAGTATTGCACTGCTGAAGA GTCACTATGAGAAAATAAAACAAATAAGACTCAAATGCTCAAAGTGCACGGGTTCTGGTTGTCTCTGCTGAGCACCG TGTGTCAATGGAGATGGCCTCTGCTGACTCAGATGAAGACCCAGGCATAAGGTGGAAAAACACCTCATTTGACCTTG CCAGCTGACCTCAAAACCTGCATTGAACCGACCAACATTAAAGTCCAGAGAGTAAACTTGAATGGAATAACGACATT CAGAAGTTAACATTGAATTCTGAACACTGGAGAAAAACGAAAAATGGACGGGGCATGAAGAGACTAACATCTGG AACCGATTTCAGTGGCGATGGCATGACAGAGCTAGAGCTGGGCCAGCCCCAGGCTGCAGCCCATTGCAGGCACCG AAAGAACCTCCCCAGTATGGTGGCTGGAAAGGACATTGGAAAGATCAACTATATCTTCTGTGCATTGGATGGAA TTTCAGTTICATCAGATGTCACCATGGCCACCCAGAACACCGAAGTAATTCCAGCATAGCGGGGAAGATGTTGACCAA GGTGGAGAAGAACAOGAAAAGGAGAAGTCACAGCACCTAGAAGGCAGGGCTCCTCTCAGCTCTGATTAGATG AAACTGTTACCTAACOCTAACACAGTATTCTTTTATTGTAATAAAAGGKAATCACAGCCACC AACATTCCAAGCTACOCTGGTACCTTGTGCAGTAGAGCTAGTGAGCATGTGAGCAAGGGTGTGCACACGGAGACT CATCGTTATAATTACTATCTGCCAAGGAGTAGAAAGAAAGGCTGGGATATTGGGTTGGCTTGGKTTTGATTTTT GCTTGGTTGGTTGGTTGKACTAAAACAGTATTATCTTTGAATATGTTAGGGACATAARKWWWWMMWKKTWWTCMAW YMRAKAKGSYWRRAWKGGSYTYSKRRKSTMWAMWYKWSMCCYSKRRWWAWTYWYWMWYCMYKYSSTGRYKRN KTAATGAAGTT	

Analysis of 23553 (871 aa)

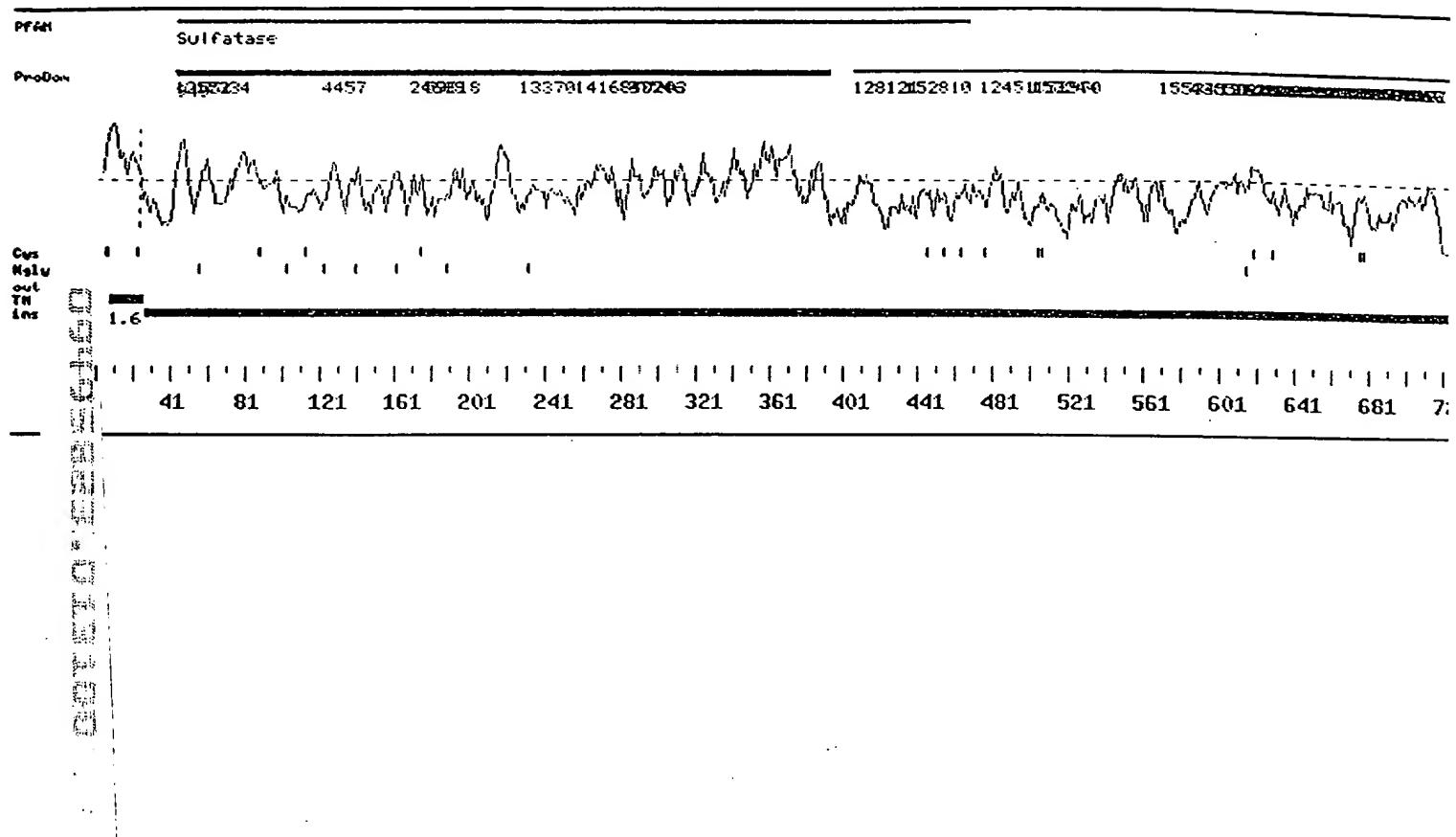


FIG 6

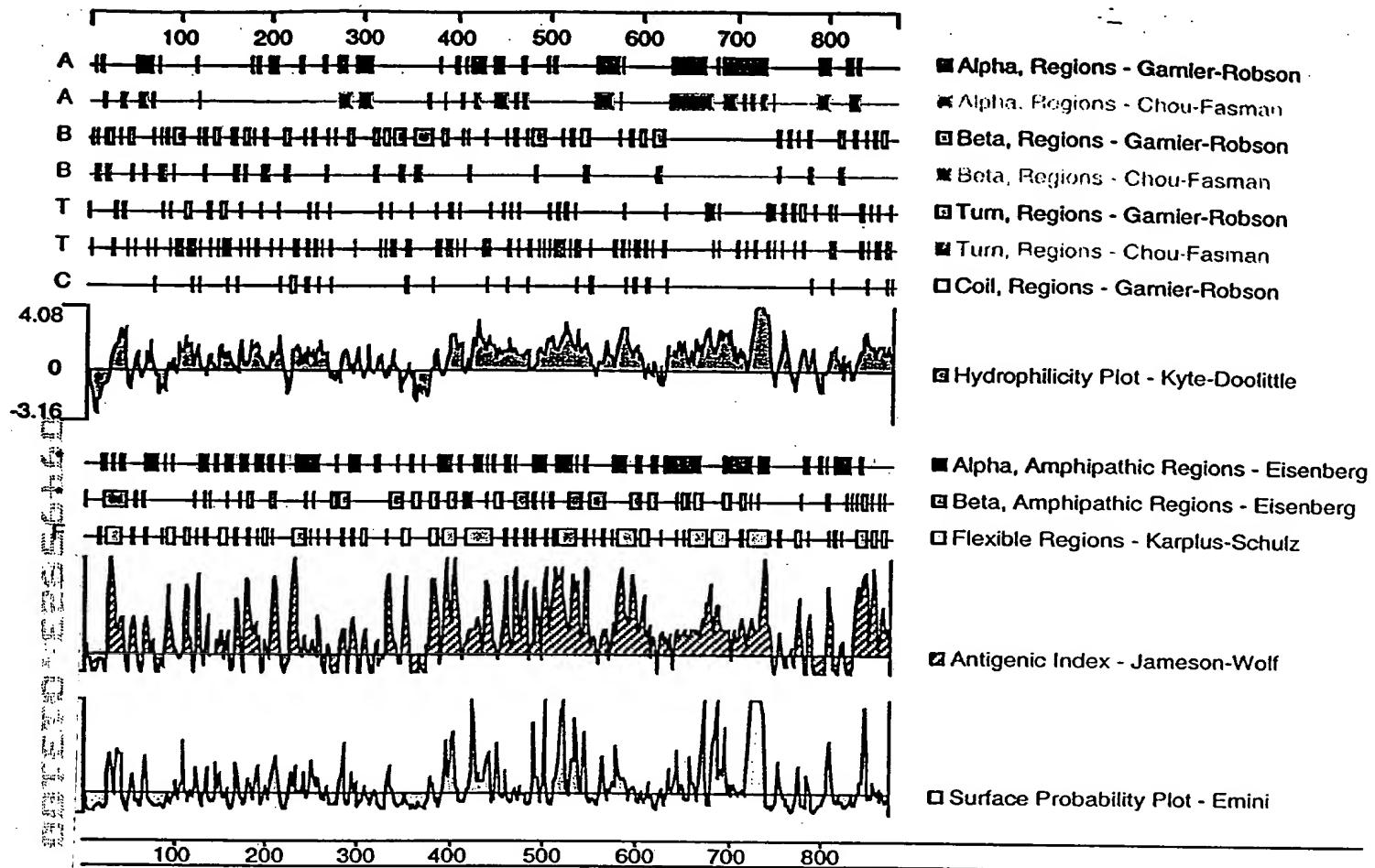


FIG 7

Prosite Pattern Matches for 23553

Prosite version: Release 12.2 of February 1995

>PS00001|PDOC00001|ASN_GLYCOSYLATION N-glycosylation site.

Query: 64	NKTR	67
Query: 111	NCSS	114
Query: 131	NNTG	134
Query: 148	NGSY	151
Query: 170	NYTV	173
Query: 197	NESI	200
Query: 240	NASQ	243
Query: 623	NDSI	626
Query: 773	NNTY	776
Query: 783	NETH	786

>PS00005|PDOC00005|PKC_PHOSPHO_SITE protein kinase C phosphorylation site.

Query: 24	TVR	26
Query: 27	SPR	29
Query: 66	TRK	68
Query: 96	TGK	98
Query: 206	SKR	208
Query: 400	TNK	402
Query: 425	SSK	427
Query: 468	SGK	470
Query: 484	TVR	486
Query: 488	STR	490
Query: 505	SCR	507
Query: 516	SQR	518
Query: 520	SQR	522
Query: 530	TPK	532
Query: 611	TVR	613
Query: 615	THK	617
Query: 635	SAR	637

>PS00006|PDOC00006|CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

Query: 107	TNNE	110
Query: 288	SVDD	291
Query: 367	TILO	370
Query: 376	TPPD	379
Query: 452	TACE	455
Query: 505	SCRE	508
Query: 781	TVNE	784

>PS00007|PDOC00007|TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.

Query: 637 RAWKDHKAY 645

>PS00008|PDOC00008|MYRISTYL N-myristoylation site.

Query: 19 GSLCST 24

Query: 161 GLIKNS 166

Query: 325 GLVKGK 330

Query: 592 GGNRGR 597

Query: 763 GSFCAC 768

Query: 851 GNKDGG 856

>PS00523|PDOC00117|SULFATASE_1 Sulfatases signature 1.

Query: 85 PMCCPSRSSMLTG 97

FIG. 8(2)

23553 Oncology Taqman

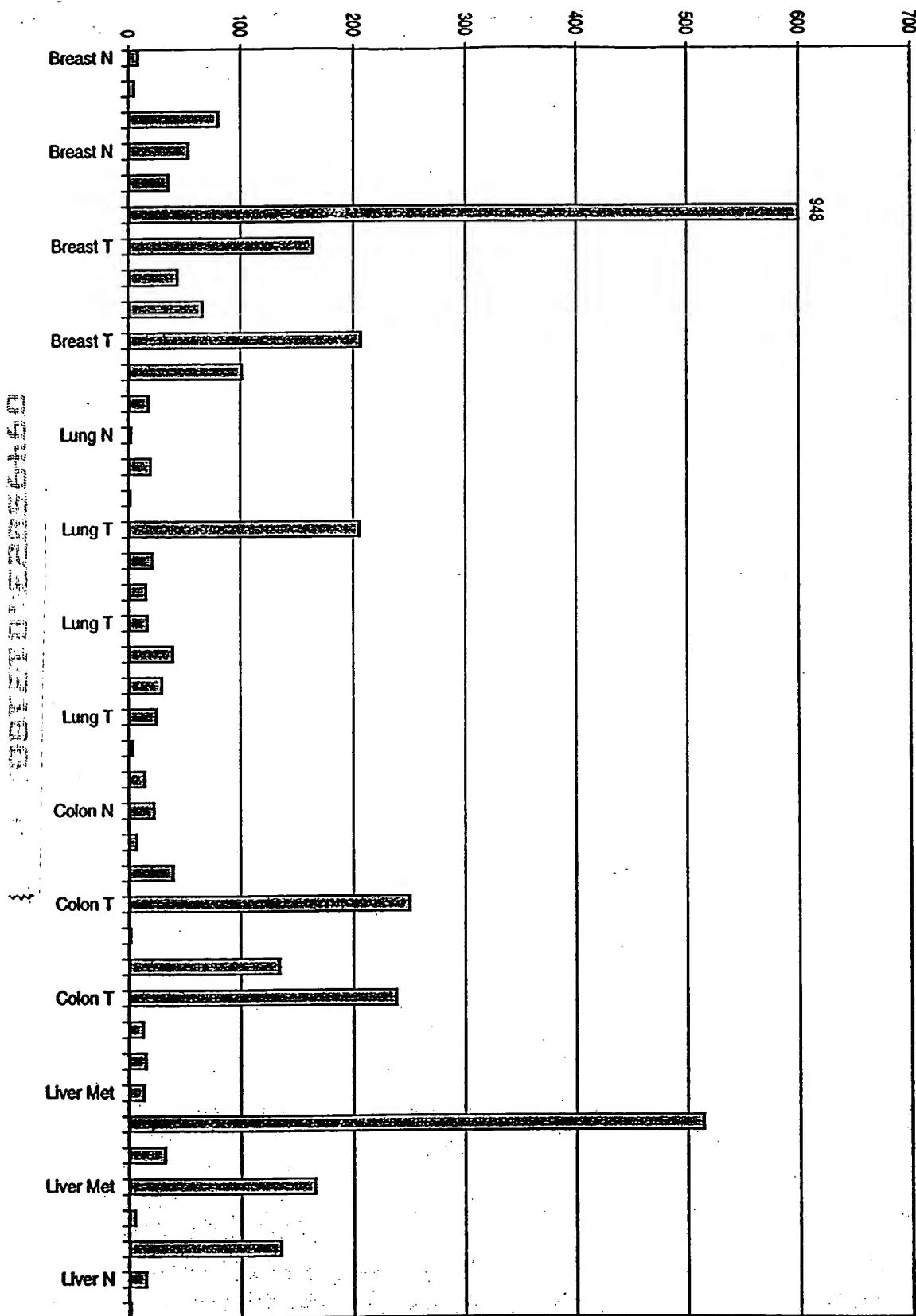


FIG 9

Input file Fbh25278FL1.seq; Output File 25278.trans
Sequence length 2940

CCAOOGGTCCGGCCAOOGGTCCGGCTGCCACGCGCGTCTCAGGCTGGCGGGCTGAGCGGGGAAGAGGGAGCAAAGG
CGCGCGAGGGCCTGGCTTACGGCAGCGGGAGGCAGCTGGCGGGGCTGAACCTCCCCAGAGGGCGGGCTGCGGCGA
GCAGATCCGGCCAGCGTCCGGCAGCCAGTCCGGACCAGACACTGGACCGTCCCCGGGGCTGAACCTCCCCAG
AGCATCCGAGCGGGGGGGGGTGGTGGCGGGCTGGGCGGGAGGTGGTGAGGCCCCAGGAGCCCCGGGGCGGGACA

M	H	T	L	T	G	F	S	L	V	S	L	L	S	F		15						
CGCGGGCGGGCTTGGCG	ATG	CAC	ACC	CTC	ACT	GGC	TTC	TCT	CTG	GTC	AGC	CTG	CTC	AGC	TTC		45					
G	Y	L	S	W	D	W	A	K	P	S	F	V	A	D	G	P	G	E	A		35	
GGC	TAC	CTG	TCC	TGG	GAC	TGG	GCC	AAG	CCG	AGC	TTC	GTG	GCC	GAC	GGG	CCC	GGG	GAG	GCT		105	
G	E	Q	P	S	A	A	P	P	Q	P	P	H	I	I	F	I	L	T	D		55	
GGC	GAG	CAG	CCC	TCG	GCC	GCT	CCG	CCC	CAG	CCT	CCC	CAC	ATC	ATC	TTC	ATC	ATC	CTC	ACG	GAC		165
D	Q	G	Y	H	D	V	G	Y	H	G	S	D	I	E	T	P	T	L	D		75	
GAC	CAA	GGC	TAC	CAC	GAC	GTG	GGC	TAC	CAT	GGT	TCA	GAT	ATC	GAG	ACC	OCT	ACG	CTG	GAC		225	
R	L	A	A	K	G	V	K	L	E	N	Y	Y	I	Q	P	I	<u>C</u>	<u>T</u>	<u>P</u>		95	
AGG	CTG	CGG	GCC	AAG	GGG	GTC	AAG	TTG	GAG	AAT	TAT	TAC	ATC	CAG	CCC	ATC	TGC	ACG	CCT		285	
S	R	S	Q	L	L	T	G	R	Y	Q	I	H	T	G	L	Q	H	S	I		115	
TCG	CGG	AGC	CAG	CTC	CTC	ACT	GGC	AGG	TAC	CAG	ATC	CAC	ACA	GGA	CTC	CAG	CAT	TCC	ATC		345	
I	R	P	Q	Q	P	N	C	L	P	L	D	Q	V	T	L	P	Q	K	L		135	
ATC	CGC	CCA	CAG	CAG	CCC	AAC	TGC	CTG	CCC	CTG	GAC	CAG	GTG	ACA	CTG	CCA	CAG	AAG	CTG		405	
Q	E	A	G	Y	S	T	H	M	V	G	K	W	H	L	G	F	<u>Y</u>	<u>R</u>	<u>K</u>		155	
CAG	GAG	GCA	GGT	TAT	TCC	ACC	CAT	ATG	GTG	GGC	AAG	TGG	CAC	CTG	GGC	TTC	TAC	CGG	AAG		465	
E	C	L	P	T	R	R	G	F	D	T	F	L	G	S	L	T	G	N	V		175	
GAG	TGT	CTG	CCC	ACC	CGT	CGG	GGC	TTC	GAC	ACC	TTC	CTG	GGC	TCG	CTC	ACG	GGC	AAT	GTG		525	
D	Y	Y	T	Y	D	N	C	D	G	P	G	V	C	G	F	D	L	H	E		195	
GAC	TAT	TAC	ACC	TAT	GAC	AAC	TGT	GAT	GGC	CCA	GGC	GTG	TGC	GGC	TTC	GAC	CTG	CAC	GAG		585	
G	E	N	V	A	W	G	L	S	G	Q	Y	S	T	M	L	Y	A	Q	R		215	
GGT	GAG	AAT	GTG	GCC	TGG	GGG	CTC	AGC	GGC	CAG	TAC	TAC	ACT	AAT	CTT	TAC	GCC	CAG	CGC		645	
A	S	H	I	L	A	S	H	S	P	Q	R	P	L	<u>F</u>	<u>L</u>	<u>Y</u>	<u>V</u>	<u>A</u>	<u>F</u>		235	
GCG	AGC	CAT	ATC	CTG	GCC	AGC	CAC	AGC	CCT	CAG	CGT	<u>CCC</u>	<u>CTC</u>	<u>TTC</u>	<u>CTC</u>	<u>TAT</u>	<u>GTG</u>	<u>GCC</u>	<u>TTC</u>		705	
Q	A	V	H	T	P	L	Q	S	P	R	E	Y	L	Y	R	Y	R	T	M		255	
CAG	GCA	GTA	CAC	ACA	CCC	CTG	CAG	TCC	CCT	CGT	GAG	TAC	CTG	TAC	CGC	TAC	CGC	ACC	ATG		765	
G	N	V	A	R	R	K	Y	A	A	M	V	T	C	<u>M</u>	<u>D</u>	<u>E</u>	<u>A</u>	<u>V</u>	<u>R</u>		275	
GCG	AAT	GTG	GCC	CGG	CGG	AAG	TAC	GGG	GCC	ATG	GTG	ACC	TGC	ATG	GAT	GAG	GCT	GTG	CGC		825	
N	I	T	W	A	L	K	R	Y	G	F	Y	N	N	S	V	I	I	F	S		295	
AAC	ATC	ACC	TGG	GCC	CTC	AAG	CGC	TAC	GGT	TTC	TAC	AAC	AAC	AGT	GTC	ATC	ATC	TTC	TOC		885	
S	<u>D</u>	<u>N</u>	<u>G</u>	<u>G</u>	<u>Q</u>	<u>T</u>	<u>F</u>	<u>S</u>	<u>G</u>	<u>G</u>	<u>S</u>	<u>N</u>	<u>W</u>	<u>P</u>	<u>L</u>	<u>R</u>	<u>G</u>	<u>R</u>	<u>K</u>		315	
AGT	GAC	AAT	GGT	GGC	CAG	ACT	TTC	TCG	GGG	GGC	AGC	AAC	TGG	CCG	CTC	CGA	GGA	CGC	AAG		945	
G	T	Y	<u>W</u>	<u>E</u>	<u>G</u>	<u>G</u>	<u>V</u>	<u>R</u>	<u>G</u>	<u>L</u>	<u>G</u>	<u>F</u>	<u>V</u>	<u>H</u>	<u>S</u>	<u>P</u>	<u>L</u>	<u>L</u>	<u>K</u>		335	
GGC	ACT	TAT	TGG	GAA	GGT	GGC	GTG	CGG	GGC	CTA	GGC	TTT	GTC	CAC	AGT	CCC	CTG	CTC	AAG		1005	

FIG 10 (-1-)

R K Q R T S R A L M H I T D W Y P I T L V 355
 CCA AAG CAA CGG ACA AGC CGG GCA CTG ATG CAC ATC ACT GAC TGG TAC CGG ACC CTG GTG 1065

G L A G G T T S A A D G L D G Y D V W P 375
 GGT CTG GCA GGT GGT ACC ACC TCA GCA GCC GAT GGG CTA GAT GCC TAC GAC GTG TGG CGG 1125

A I S E G R A S P R T E I L H N I D P L 395
 GCC ATC AGC GAG GGC CGG GCC TCA CCA CGC ACG GAG ATC CTG CAC AAC ATT GAC CCA CTC 1185

Y N H A Q H G S L E G G F G I W N T A V 415
 TAC AAC CAT GCC CAG CAT GGC TCC CTG GAG GGC GGC TTT GGC ATC TGG AAC ACC GCC GTG 1245

Q A A I R V G E W K L L T G D P G Y G D 435
 CAG GCT GCC ATC CGC GTG GGT GAG TGG AAG CTG CTG ACA GGA GAC CCC GGC TAT GGC GAT 1305

W I P P Q T L A T F P G S W W N L E R M 455
 TGG ATC CCA CCG CAG ACA CTG GCC ACC TTC CCG GGT AGC TGG TGG AAC CTG GAA CGA ATG 1365

A S V R Q A V W L F N I S A D P Y E R E 475
 GCC AGT GTC CGC CAG GCC GTG TGG CTC TTC AAC ATC AGT GCT GAC CCT TAT GAA CGG GAG 1425

D L A G Q R P D V V R T L L A R L A E Y 495
 GAC CTG GCT GGC CAG CGG CCT GAT GTG GTC CGC ACC CTG CTG GCT CGC CTG GCC GAA TAT 1485

N R T A I P V R Y P A E N P R A H P D F 515
 AAC CGC ACA GCC ATC CCG GTA CGC TAC CCA GCT GAG AAC CCC CGG GCT CAT CCT GAC TTT 1545

N G G A W G P W A S D E E E E E E E G R 535
 AAT GGG GGT GCT TGG GGG CCC TGG GCC AGT GAT GAG GAA GAG GAG GAA GAG GGG AGG 1605

A R S F S R G R R K K K C K I C K L R S 555
 GCT CGA AGC TTC TCC CGG GGT CGT CGC AAG AAA AAA TGC AAG ATT TGC AAG CTT CGA TCC 1665

F F R K L N T R L M S Q R I * 570
 TTT TTC CGT AAA CTC AAC ACC AGG CTA ATG TCC CAA CGG ATC TGA 1710

TGGTGGGGAGGGAGAAAATGTCCCTTAAGAGGATCTTCCCCACTCCGGCTTGGCCCTGCTGTTCTCAGGGAGAAGCCT
 GTCACATCTCCATCTACAGGGAGTTGGAGGGTGTAGAGTCCCTTGGTGAACAGGGTAGGGAGCCTGGATAGGAGTGGG
 TGGGAATAAACCAAGACTGGGATGCTGTCTCAGTCTGCTOCTCACGGACTTGCTCTGTGACCTCAGGTGACCCAC
 ATGACCTTTAGCCTCAGTTCTCATCTGAAAATGAGCTCTAATGACTTTGTGACTCTTGGTGTGGCCCTGGAGCC
 TGGGGCCACGGTGGAGTTCCCTGGCCGGCCTTGOCACCTGACAACCTTAAAGGCTTCCCCCTTAACAOGGGATCCCTG
 TGGTGGTGTGTTGGGAGTGGCTGGAGGCAACTOCAAGGCTGGGCCCCCAGCTGAAGCATGGCAATCTGGCTGCTCTAC
 AGGGACCCCCAAGGCTGTGGGTGGAGGGCAGGGTGGGGGGTGTGACCTTCTGGGTCTTACATGGCTAGGCCAG
 TCCCTGGCTCAGACTGGTGTCAAGGCAACGGTGGCAAAATCCCTTCTGGCCCTCCAGTACCCAGAGAAACTGGCTG
 GGCCATTAACGTGCTGCAGCACCAAGGGTGGTAGAAAGAGCTGTGAAGAGGCCCCAAACCAAGTACCCAGGACACCTGGGTT
 CTGGTGTGACCTGGGACAGTTCTTCCCTCTAAGGCTTGTGATTTCCCCACCTGCAAGTGGGATGCCAGGGCTGGCTC
 TGCCCTTCAATGAGGCTCTGGAAGACTGGCAAGGTTGTGGAGGAGCTTGTGAACATGATTAAGTGTGTAACATGG
 AAAAAAAAAAAAAAAAAAAAAAGGGGGG

Analysis of 25278 (569 aa)

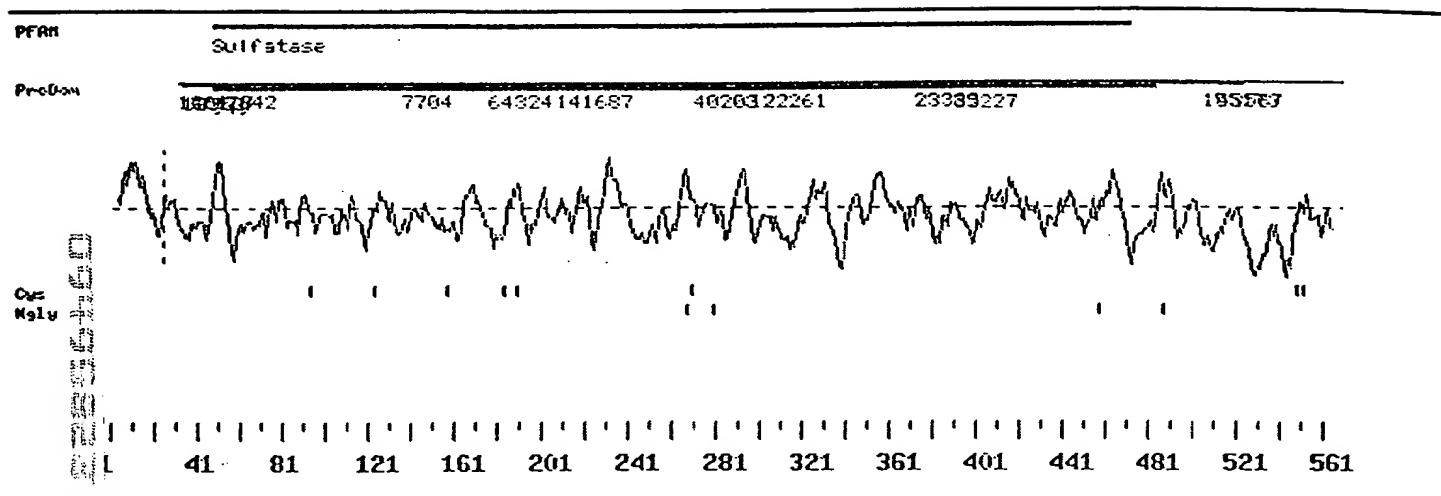


FIG-11

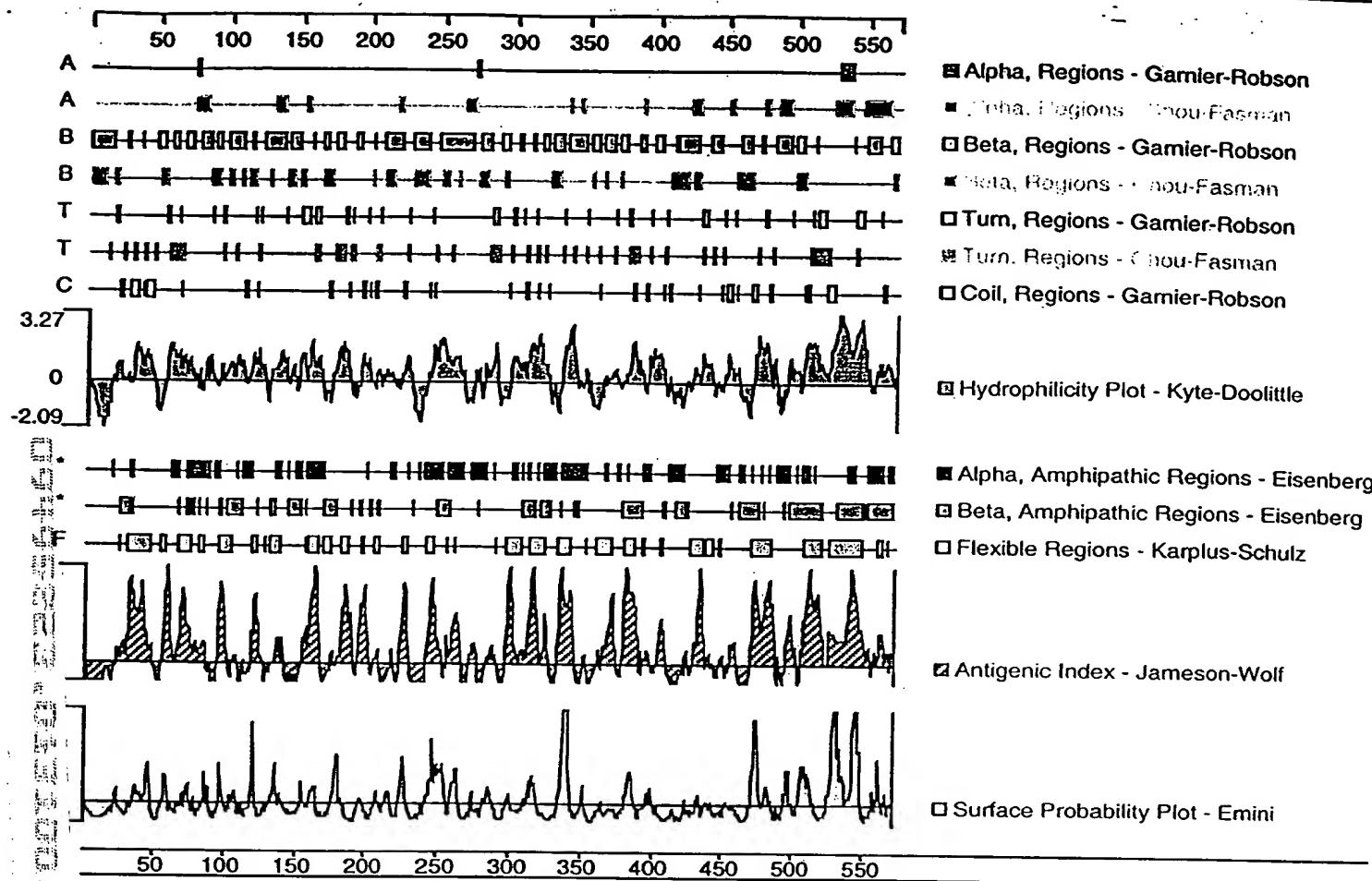


FIG 12

Prosite Pattern Matches for 2578

Prosite version: Release 12.2 of February 1995

>PS00001|PDOC00001|ASN_GLYCOSYLATION N-glycosylation site.

Query: 276 MITW 279
Query: 288 MRSV 291
Query: 466 NISA 469
Query: 496 NRTA 499

>PS00004|PDOC00004|CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.

Query: 314 RKGT 317

>PS00005|PDOC00005|PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.

Query: 102 TGR 104
Query: 160 TRR 162
Query: 244 SPR 246
Query: 340 TSR 342
Query: 383 SPR 385
Query: 457 SVR 459
Query: 566 SQR 568

>PS00006|PDOC00006|CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

Query: 67 SDIE 70
Query: 244 SPRE 247
Query: 268 TCMD 271
Query: 317 TYWE 320
Query: 363 SAAD 366
Query: 525 SDEE 528

>PS00007|PDOC00007|TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.

Query: 134 KLQEAGY 140

>PS00008|PDOC00008|MYRISTYL N-myristoylation site.

Query: 110 GLQHSI 115
Query: 169 GSLTGN 174
Query: 205 GQYSTM 210
Query: 300 GQTFSG 305
Query: 321 GGVRGL 326
Query: 356 GLAGGT 361
Query: 402 GSLEGG 407
Query: 409 GIWNTA 414
Query: 447 GSWWNL 452

>PS00009|PDOC00009|AMIDATION Amidation site.

Query: 312 RGRK 315
Query: 541 RGRR 544

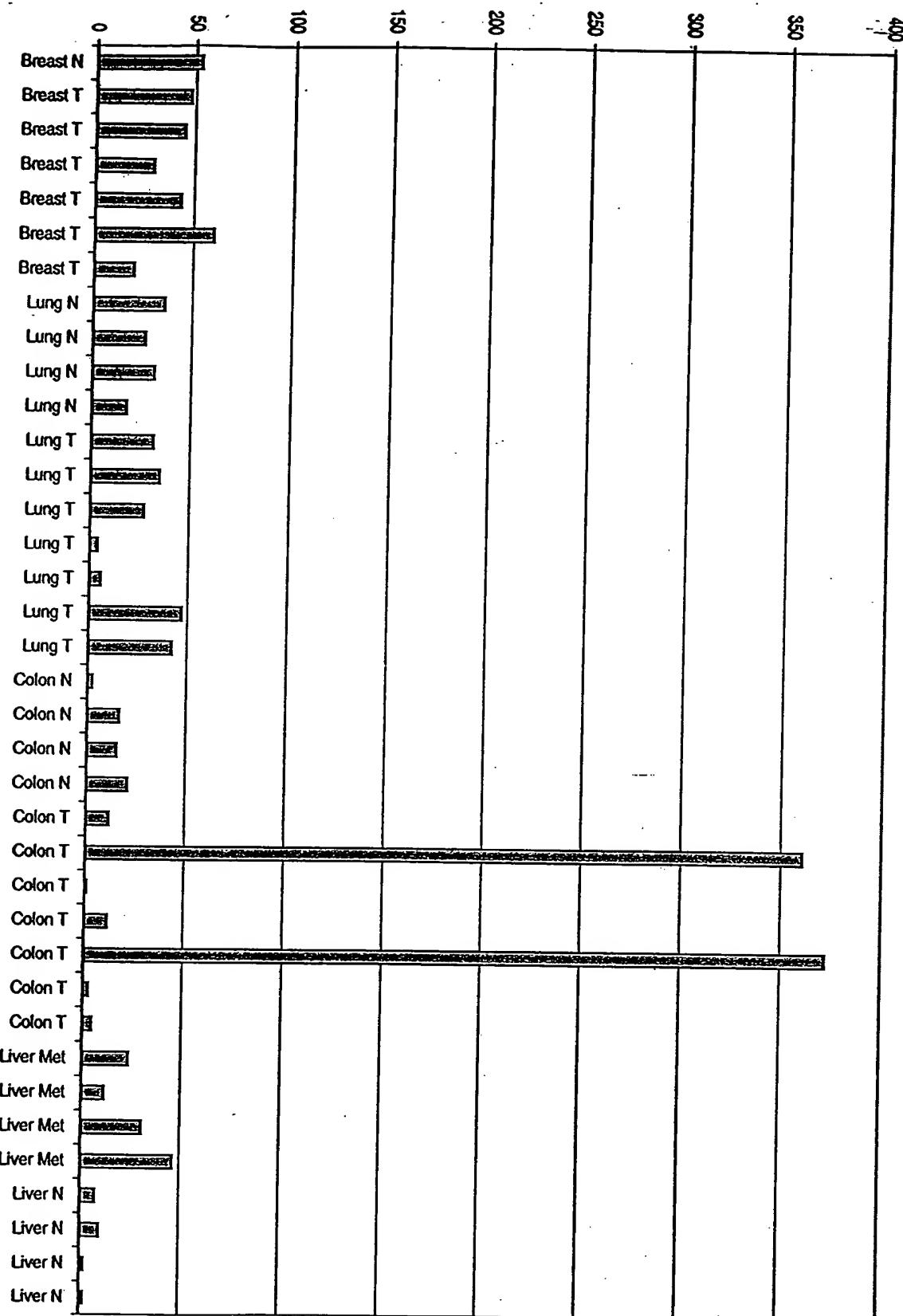
>PS00017|PDOC00117|SULFATASE_2 Sulfatases signature 2.

Query: 139 GYSTHMVGKW 148

>PS00523|PDOC00117|SULFATASE_1 Sulfatases signature 1.

Query: 91 PICTPSRSQLLTG 103

FIG 13



25278 Oncology Taqman

FIG 14

Input file 26212cons; Output File 26212pat
Sequence length 2266

CACCGCGTCCGCCACCGCGTCCGTGGAGATATTAACTTTTCTTTTTTTCTGGTGGAAAGCTGCTCTAGGGAGG
GGGGAGGAGGAGGAGAAGTGAATGTGCTGGAGAAGAGCGAGCCCTCCTGTCTTCCGGAGTCCCATCCATTAAGCC
ATCACTCTGGAAGATTAAGTTGTCGGACATGGTACAGCTGAGAGGGAGGAGGAGGAGTCTTGCAGGTGGAGAGTCT
TCACCGTCTGTTGGGTGCATGTGCGCCCGCASCGGCGGGGGCGCGTGGTCTCCGCGTGGAGTCTCACCTGGGACC

M	A	P	R	G	C	A	G	H	P	P	P	S	P	Q	A	C	18				
TGAGTGA	ATG	GCT	CCC	AGG	GGC	TGT	GCG	GGG	CAT	CCG	CCT	CCG	CCT	TCT	CCA	CAG	GCC	TGT	54		
V	C	P	G	K	M	L	A	M	G	A	L	A	G	F	W	I	L	C	L	38	
GTC	TGT	CCT	GGG	AAG	ATG	CTA	GCA	ATG	GGG	GCG	CTG	GCA	GGA	TTC	TGG	ATC	CTC	TGC	CTC	114	
L	T	Y	G	Y	L	S	W	G	Q	A	L	E	E	E	E	E	G	A	L	58	
CTC	ACT	TAT	GGT	TAC	CTG	TCC	TGG	GGC	CAG	GCC	TTA	GAA	GAG	GAG	GAA	GAA	GGG	GCC	TTA	174	
L	A	Q	A	G	E	K	L	E	P	S	T	T	S	T	S	Q	P	H	L	78	
GTC	GCT	CAA	GCT	GGG	GAG	AAA	CTA	GAG	CCC	AGC	ACA	ACT	TCC	ACC	TCC	CAG	CCC	CAT	CTC	234	
G	I	F	I	L	A	D	D	Q	G	F	R	D	V	G	Y	H	G	S	E	I	98
GAT	TTC	ATC	CTA	GCG	GAT	GAT	CAG	GGG	TTT	AGA	GAT	GTG	GGT	TAC	CAC	GGA	TCT	GAG	ATT	294	
T	P	T	L	D	K	L	A	A	E	G	V	K	L	E	N	Y	Y	V	118		
A	ACA	CCT	ACT	CTT	GAC	AAG	CTC	GCT	GCC	GAA	GGG	GTT	AAA	CTG	GAG	AAC	TAC	TAT	GTC	354	
P	I	C	T	P	S	R	S	Q	F	I	T	G	K	Y	Q	I	H	T	138		
G	CCT	ATT	TGC	ACA	CCA	TCC	AGG	AGT	CAG	TTT	ATT	ACT	GGA	AAG	TAT	CAG	ATA	CAC	ACC	414	
L	Q	H	S	I	I	R	P	T	Q	P	N	C	L	P	L	D	N	A	158		
A	CTT	CAA	CAT	TCT	ATC	ATA	AGA	CCT	ACC	CAA	CCC	AAC	TGT	TTA	CCT	CTG	GAC	AAT	GCC	474	
L	P	Q	K	L	K	E	V	G	Y	S	T	H	M	V	G	K	W	H	178		
C	CTA	CCT	CAG	AAA	CTG	AAG	GAG	GTT	GGA	TAT	TCA	ACG	CAT	ATG	GTC	GGA	AAA	TGG	CAC	534	
G	F	Y	R	K	E	C	M	P	T	R	R	G	F	D	T	F	F	G	198		
G	GGT	TTT	TAC	AGA	AAA	GAA	TGC	ATG	CCC	ACC	AGA	AGA	GGA	TTT	GAT	ACC	TTT	TTT	GGT	594	
L	L	G	S	G	D	Y	Y	T	H	Y	K	C	D	S	P	G	M	C	218		
C	CTT	TTG	GGA	AGT	GGG	GAT	TAC	TAT	ACA	CAC	TAC	AAA	TGT	GAC	AGT	CCT	GGG	ATG	TGT	654	
Y	D	L	Y	E	N	D	N	A	A	W	D	Y	D	N	G	I	Y	S	238		
C	TAT	GAC	TTG	TAT	GAA	AAC	GAC	AAT	GCT	GCC	TGG	GAC	TAT	GAC	AAT	GGC	ATA	TAC	TCC	714	
Q	O	M	Y	T	Q	R	V	Q	Q	I	L	A	S	H	N	P	T	K	P	258	
ACA	CAG	ATG	TAC	ACT	CAG	AGA	GTA	CAG	CAA	ATC	TTA	GCT	TCC	CAT	AAC	CCC	ACA	AAG	CCT	774	
I	F	L	Y	I	A	Y	Q	A	V	H	S	P	L	Q	A	P	G	R	Y	278	
ATA	TTT	TTA	TAT	ATT	GCC	TAT	CAA	GCT	GTT	CAT	TCA	CCA	CTG	CAA	GCT	CCT	GGC	AGG	TAT	834	
F	E	H	Y	R	S	I	I	N	I	N	R	R	R	Y	A	A	M	L	S	298	
TTC	GAA	CAC	TAC	CGA	TCC	ATT	ATC	AAC	ATA	AAC	AGG	AGG	AGA	TAT	GCT	GCC	ATG	CTT	TCC	894	
C	L	D	E	A	I	N	N	V	T	L	A	L	K	T	Y	G	F	X	N	318	
TGC	TTA	GAT	GAA	GCA	ATC	AAC	AAC	GTG	ACA	TTG	GCT	CTA	AAG	ACT	TAT	GGT	TTC	TAT	AAC	954	
N	S	I	I	I	Y	S	S	D	N	G	G	Q	P	T	A	G	G	S	N	338	
AAC	AGC	ATT	ATC	ATT	TAC	TCT	TCA	GAT	AAT	GGT	GGC	CAG	CCT	ACG	GCA	GGA	GGG	AGT	AAC	1014	
W	P	L	R	G	S	K	G	T	Y	W	E	G	G	I	R	A	V	G	F	358	
TGG	CCT	CTC	AGA	GGT	AGC	AAA	GGA	ACA	TAT	TGG	GAA	GGG	ATC	CGG	GCT	GTA	GGC	TTT	1074		

V	H	S	P	L	L	K	N	K	G	T	V	C	K	E	L	V	H	I	T	378
GTC	CAT	AGC	CCA	CTT	CTG	AAA	AAC	AAG	GGA	ACA	GTG	TGT	AAG	GAA	CTT	GTG	CAC	ATC	ACT	1134
D	W	Y	P	T	L	I	S	L	A	E	G	Q	I	D	E	D	I	Q	L	398
GAC	TGG	TAC	CCC	ACT	CTC	ATT	TCA	CTG	GCT	GAA	GGA	CAG	ATT	GAT	GAG	GAC	ATT	CAA	CTA	1194
D	G	Y	D	I	W	E	T	I	S	E	G	L	R	S	P	R	V	D	I	418
GAT	GGC	TAT	GAT	ATC	TGG	GAG	ACC	ATA	AGT	GAG	GGT	CTT	CGC	TCA	CCC	CGA	GTA	GAT	ATT	1254
L	H	N	I	D	P	I	Y	T	K	A	K	N	G	S	W	A	A	G	Y	438
TTG	CAT	AAC	ATT	GAC	CCC	ATA	TAC	ACC	AAG	GCA	AAA	AAT	GCG	TCC	TGG	GCA	GCA	GGC	TAT	1314
G	I	W	N	T	A	I	Q	S	A	I	R	V	Q	H	W	K	L	L	T	458
GGG	ATC	TGG	AAC	ACT	GCA	ATC	CAG	TCA	GCC	ATC	AGA	GTG	CAG	CAC	TGG	AAA	TTG	CTT	ACA	1374
G	N	P	G	Y	S	D	W	V	P	P	Q	S	F	S	N	L	G	P	N	478
GGA	AAT	CCT	GGC	TAC	AGC	GAC	TGG	GTC	CCC	CCT	CAG	TCT	TTC	AGC	AAC	CTG	GGA	CCG	AAC	1434
R	W	H	N	E	R	I	T	S	S	T	G	K	S	V	W	L	F	N	I	498
CGG	TGG	CAC	AAT	GAA	CGG	ATC	ACC	TCG	TCA	ACT	GGC	AAA	AGT	GTA	TGG	CTT	TTC	AAC	ATC	1494
T	A	D	P	Y	E	R	V	D	L	S	N	R	Y	P	G	I	V	K	K	518
ACA	GCC	GAC	CCA	TAT	GAG	AGG	GTG	GAC	CTA	TCT	AAC	AGG	TAT	CCA	GGA	ATC	GTG	AAG	AAG	1554
L	R	R	L	S	Q	F	N	K	T	A	V	P	V	R	Y	P	P	K	538	
CTA	CGG	AGG	CTC	TCA	CAG	TTC	AAA	ACT	GCA	GTG	CCG	GTC	AGG	TAT	CCC	CCC	AAA		1614	
P	R	S	N	P	R	L	N	G	G	V	*									551
CCC	AGA	AGT	AAC	CCT	AGG	CTC	AAT	GGA	GGG	GTC	TAG									1653
ACCATGGTATAAGAGAGGAAACCAAGAAAAAGAAGCCAAGCAAAATCAGGCTGAGAAAAAGCAAAAGAAAAGCAAA																				
AGAAGAAGAAACAGCAGAAAGCAGTCTCAGGTTCAACTTGCCATTAGGTGTACTTGTGGATAAGCACAAATATT																				
TGTTGGTTAAACTTAATCAGTTCTTATCTTCATCTGTTCTAGGTAAACCAGCAAATTGGCTCGATAATATC																				
GGCCTAACCGTCAGGTTGTTCATGCTGTGCCACCTGGTGCCGAATT																				

Analysis of 26212prot (550 aa)

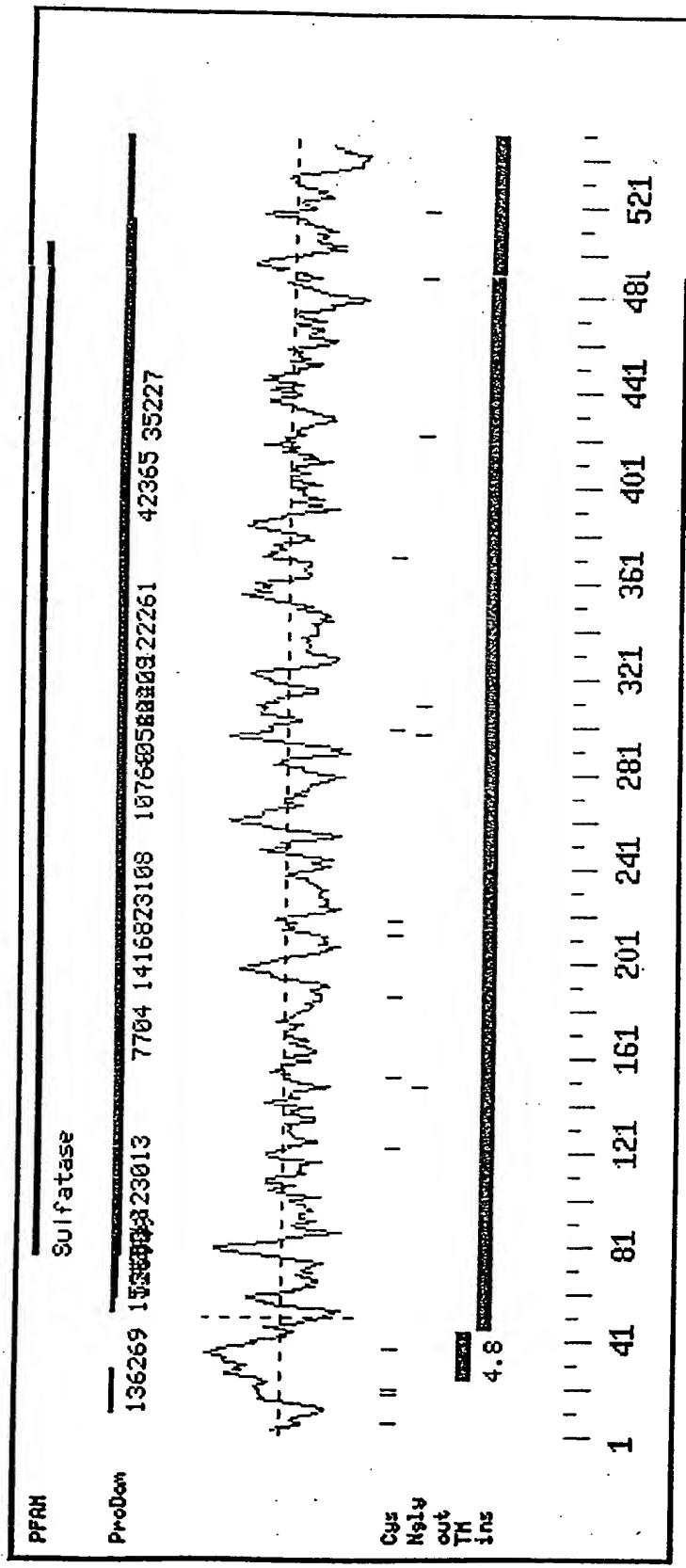


Fig. 16

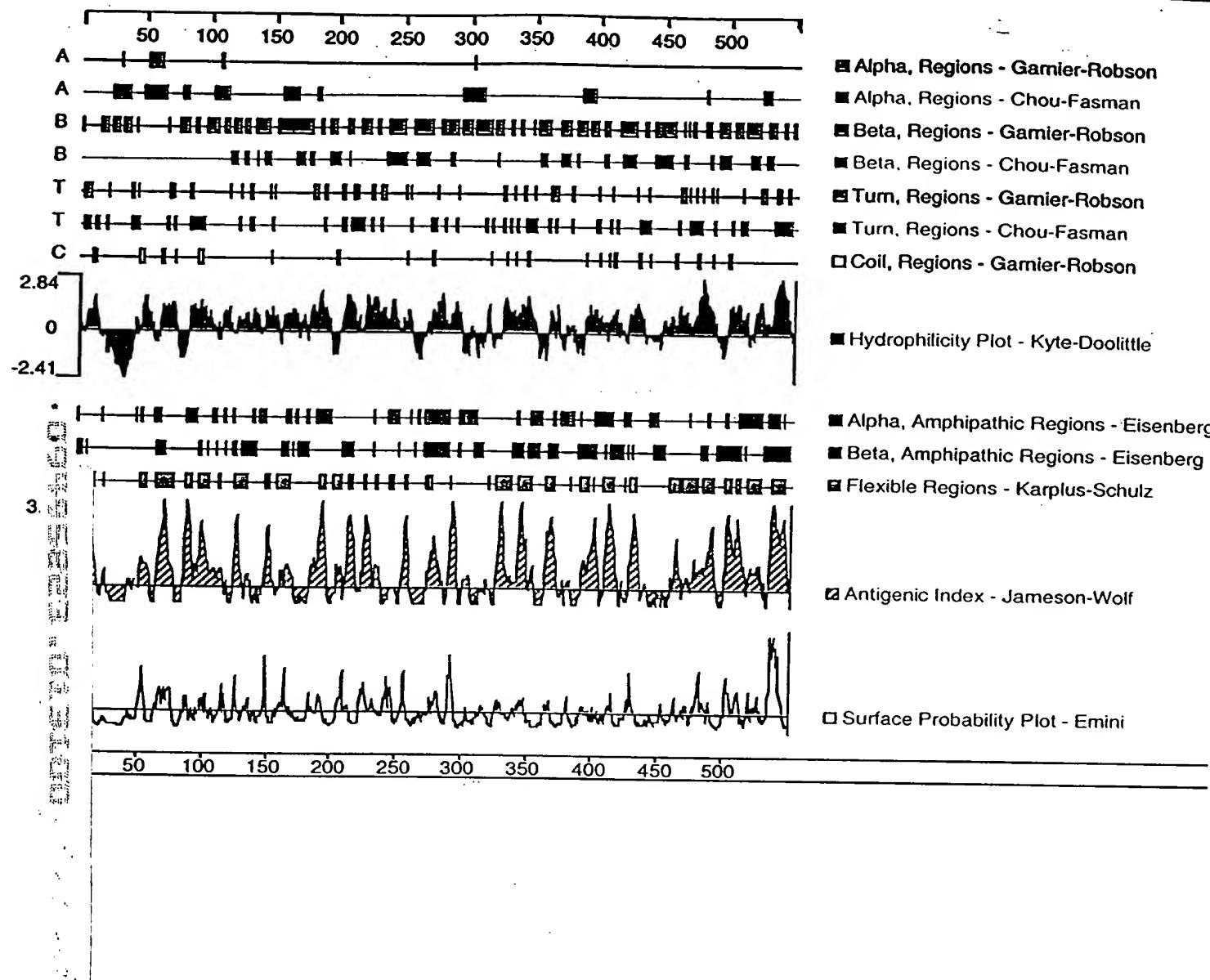


FIG 17

Prosite Pattern Machines for 26212prot

Prosite version: Release 12.2 of February 1995

>PS00001|PDOC00001|ASN_GLYCOSYLATION N-glycosylation site.

Query: 157 NATL 160

Query: 306 NVTL 309

Query: 318 NNSI 321

Query: 431 NGSW 434

Query: 497 NITA 500

Query: 527 NKTA 530

>PS00004|PDOC00004|CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.

Query: 521 RRLS 524

>PS00005|PDOC00005|PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.

Query: 131 TGK 133

Query: 189 TRR 191

Query: 243 TQR 245

Query: 413 SPR 415

Query: 489 TGK 491

Query: 509 SNR 511

>PS00006|PDOC00006|CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

Query: 298 SCLD 301

Query: 347 TYWE 350

Query: 386 SLAE 389

Query: 406 TISE 409

>PS00007|PDOC00007|TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site.

Query: 163 KLKEVGY 169

>PS00008|PDOC00008|MYRISTYL N-myristoylation site.

Query: 28 GALAGF 33

Query: 56 GALLAQ 61

Query: 139 GLQHSI 144

Query: 198 GSLLGS 203
Query: 235 GIYSTQ 240
Query: 329 GGQPTA 334
Query: 343 GSKGTY 348
Query: 351 GGIRAV 356
Query: 432 GSWAAG 437
Query: 439 GIWNTA 444

>PS00149 | PDOC00117 | SULFATASE_2 Sulfatases signature 2.

Query: 168 GYSTHMVGKW 177

>PS00523 | PDOC00117 | SULFATASE_1 Sulfatases signature 1.

Query: 120 PICTPSRSQFITG 132